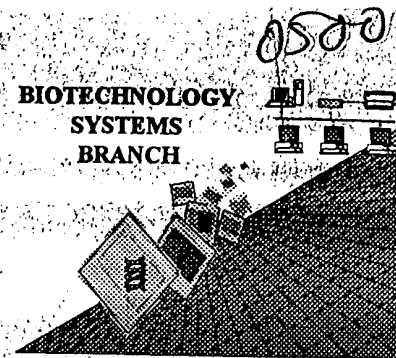# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: _09/513,999_

Art Unit / Team No.: _OIPE_

Date Processed by STIC: _3/16/2000_

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** SERIAL NUMBER: _09/573999_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

15-16 (maybe more)

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain sourc of genetic material in <220> t <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please d not use "Copy t Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, pleas us "File Manager" or any other means to copy file t floppy disk.
AKS-Biotechnology Systems Branch- 5/15/99

> This Raw Listing contains the General
> Information Section and those Sequences
> containing ERRORS.

Does Not Comply
Corrected Diskette Needed

```
 1   <110>  Dumas Milne Edwards, J.B.
 2          Duclert A.
 3          Giordano, J.Y.
 4   <120>  Expressed Sequence Tags and Encoded Human Proteins.
 5   <130>  GENSET.054A
 6   <150>  US 60/122,487
 7   <151>  1999-02-26
 8   <160>  36681
 9   <170>  Patent.pm
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Due to size of listing, the following pages shown as samples of global errors. Please

ERRORED SEQUENCES FOLLOW

check all sequences to ensure <211> responses match actual number of bases/amino acids shown.

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       10    <210>  8
E-->   11    <211>  681  227 shown
       12    <212>  PRT
       13    <213>  Homo sapiens
       14    <220>
       15    <221>  SIGNAL
       16    <222>  -22..-1
       17    <223>  score 8.5
       18           seq AALLLGLMMVVTG/DE
       19    <400>  8
       20           Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
       21                   -20                 -15                 -10
       22           Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
       23                -5                   1               5                   10
       24           Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
       25                           15                  20                  25
       26           Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
       27                       30                  35                  40
       28           Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
       29                       45                  50                  55
       30           Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
       31                   60                  65                  70
       32           Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
       33               75                  80                  85                  90
       34           Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile
       35                           95                  100                 105
       36           Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
       37                       110                 115                 120
       38           Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys
       39                       125                 130                 135
```

```
40          Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys
41              140                 145                 150
42          Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser
43              155                 160                 165                 170
44          Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala
45                          175                 180                 185
46          Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile
47                          190                 195                 200
48          Ala Ala Cys
49                  205
```

```
50  <210> 10
E-->.  51  <211> 507  169 stous
52  <212> PRT
53  <213> Homo sapiens
54  <220>
55  <221> SIGNAL
56  <222> -88..-1
57  <223> score 6.7
58        seq VFALSSFLNKASA/VY
59  <400> 10
60          Met Lys Gly Gly Ile Ser Asn Val Trp Phe Asp Arg Phe Lys Ile Thr
61                          -85                 -80                 -75
62          Asn Asp Cys Pro Glu His Leu Glu Ser Ile Asp Val Met Cys Gln Val
63                  -70                 -65                 -60
64          Leu Thr Asp Leu Ile Asp Glu Glu Val Lys Ser Gly Ile Lys Lys Asn
65              -55                 -50                 -45
66          Arg Ile Leu Ile Gly Gly Phe Ser Met Gly Gly Cys Met Ala Met His
67          -40                 -35                 -30                 -25
68          Leu Ala Tyr Arg Asn His Gln Asp Val Ala Gly Val Phe Ala Leu Ser
69                          -20                 -15                 -10
70          Ser Phe Leu Asn Lys Ala Ser Ala Val Tyr Gln Ala Leu Gln Lys Ser
71                          -5                  1                   5
72          Asn Gly Val Leu Pro Glu Leu Phe Gln Cys His Gly Thr Ala Asp Glu
73              10                  15                  20
74          Leu Val Leu His Ser Trp Ala Glu Glu Thr Asn Ser Met Leu Lys Ser
75              25                  30                  35                  40
76          Leu Gly Val Thr Thr Lys Phe His Ser Phe Pro Asn Val Tyr His Glu
77                          45                  50                  55
78          Leu Ser Lys Thr Glu Leu Asp Ile Leu Lys Leu Trp Ile Leu Thr Lys
79                          60                  65                  70
80          Leu Pro Gly Glu Met Glu Lys Gln Lys
81                  75                  80
```

```
82  <210> 12          327
E-->  83  <211> 981
84  <212> PRT
85  <213> Homo sapiens
86  <220>
87  <221> SIGNAL
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 89    <223> score 5.6
 90          seq ACLSLGFFSLLWL/QL
 91    <400> 12
 92          Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp Gly
 93                          -45                 -40                 -35
 94          Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser Val Phe
 95                      -30                 -25                 -20
 96          His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser Leu Leu Trp
 97                  -15                 -10                 -5
 98          Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala Val Arg Gly Gln
 99               1               5               10                  15
100          Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro
101                      20                  25                  30
102          Pro Glu His Trp Glu Glu Asp Ala Ser Trp Gly Pro His Arg Leu Ala
103                      35                  40                  45
104          Val Leu Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val
105                      50                  55                  60
106          Pro His Met Arg Arg Phe Leu Ser Arg Lys Lys Ile Arg His His Ile
107               65                  70                  75
108          Tyr Val Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu
109          80                  85                  90                  95
110          Ile Asn Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala
111                      100                 105                 110
112          Met His Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly
113                      115                 120                 125
114          Phe Pro Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro
115                      130                 135                 140
116          Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys
117               145                 150                 155
118          Gln His Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp
119          160                 165                 170                 175
120          Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu
121                      180                 185                 190
122          Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe Arg
123                      195                 200                 205
124          His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala
125                      210                 215                 220
126          Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn
127                      225                 230                 235
128          Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu Ser Val Gly Gly
129          240                 245                 250                 255
130          Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp Cys Asp Lys Thr Ala
131                      260                 265                 270
132          Thr Pro Trp Cys Thr Phe Ser
133                      275
```
_____

```
134    <210> 14   395 shown
135    <211> 1185
136    <212> PRT
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137   <213> Homo sapiens
138   <220>
139   <221> SIGNAL
140   <222> -310..-1
141   <223> score 4.4
142   seq VLILLFSLALIIL/PS
143   <400> 14
144   Met Asp Leu Gly Ile Pro Asp Leu Leu Asp Ala Trp Leu Glu Pro Pro
145   -310   -305   -300   -295
146   Glu Asp Ile Phe Ser Thr Gly Ser Val Leu Glu Leu Gly Leu His Cys
147   -290   -285   -280
148   Pro Pro Pro Glu Val Pro Val Thr Arg Leu Gln Glu Gln Gly Leu Gln
149   -275   -270   -265
150   Gly Trp Lys Ser Gly Gly Asp Arg Gly Cys Gly Leu Gln Glu Ser Glu
151   -260   -255   -250
152   Pro Glu Asp Phe Leu Lys Leu Phe Ile Asp Pro Asn Glu Val Tyr Cys
153   -245   -240   -235
154   Ser Glu Ala Ser Pro Gly Ser Asp Ser Gly Ile Ser Glu Asp Ser Cys
155   -230   -225   -220   -215
156   His Pro Asp Ser Pro Pro Ala Pro Arg Ala Thr Ser Ser Pro Met Leu
157   -210   -205   -200
158   Tyr Glu Val Val Tyr Glu Ala Gly Ala Leu Glu Arg Met Gln Gly Glu
159   -195   -190   -185
160   Thr Gly Pro Asn Val Gly Leu Ile Ser Ile Gln Leu Asp Gln Trp Ser
161   -180   -175   -170
162   Pro Ala Phe Met Val Pro Asp Ser Cys Met Val Ser Glu Leu Pro Phe
163   -165   -160   -155
164   Asp Ala His Ala His Ile Leu Pro Arg Ala Gly Thr Val Ala Pro Val
165   -150   -145   -140   -135
166   Pro Cys Thr Thr Leu Leu Pro Cys Gln Thr Leu Phe Leu Thr Asp Glu
167   -130   -125   -120
168   Glu Lys Arg Leu Leu Gly Gln Glu Gly Val Ser Leu Pro Ser His Leu
169   -115   -110   -105
170   Pro Leu Thr Lys Ala Glu Glu Arg Val Leu Lys Lys Val Arg Arg Lys
171   -100   -95   -90
172   Ile Arg Asn Lys Gln Ser Ala Gln Asp Ser Arg Arg Arg Lys Lys Glu
173   -85   -80   -75
174   Tyr Ile Asp Gly Leu Glu Ser Arg Val Ala Ala Cys Ser Ala Gln Asn
175   -70   -65   -60   -55
176   Gln Glu Leu Gln Lys Lys Val Gln Glu Leu Glu Arg His Asn Ile Ser
177   -50   -45   -40
178   Leu Val Ala Gln Leu Arg Gln Leu Gln Thr Leu Ile Ala Gln Thr Ser
179   -35   -30   -25
180   Asn Lys Ala Ala Gln Thr Ser Thr Cys Val Leu Ile Leu Leu Phe Ser
181   -20   -15   -10
182   Leu Ala Leu Ile Ile Leu Pro Ser Phe Ser Pro Phe Gln Ser Arg Pro
183   -5   1   5   10
184   Glu Ala Gly Ser Glu Asp Tyr Gln Pro His Gly Val Thr Ser Arg Asn
185   15   20   25
186   Ile Leu Thr His Lys Asp Val Thr Glu Asn Leu Glu Thr Gln Val Val

187				30				35				40			
188	Glu	Ser	Arg	Leu	Arg	Glu	Pro	Pro	Gly	Ala	Lys	Asp	Ala	Asn	Gly	Ser
189				45				50				55			
190	Thr	Arg	Thr	Leu	Leu	Glu	Lys	Met	Gly	Gly	Lys	Pro	Arg	Pro	Ser	Gly
191				60				65				70			
192	Arg	Ile	Arg	Ser	Val	Leu	His	Ala	Asp	Glu	Met				
193				75				80				85			

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     194    <210> 48
E--     195    <211> 361
     196    <212> DNA
     197    <213> Homo sapiens
     198    <220>
     199    <221> CDS
     200    <222> 63..359
     201    <221> sig_peptide
     202    <222> 63..119
     203    <223> score 10.8
     204          seq ILFLVAAATGAHS/QV
     205    <400> 48
W-->  206    gagcatcacc cagcaaccac atctgtnctc tagagaatcc cctgasagct ccgttcctca     60
     207    cc atg gac tgg acc tgg agg atc ctc ttc ttg gtg gca gca gcc acm    107
     208       Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr
     209                         -15                  -10                 -5
     210    gga gcc cac tcc cag gtg crr ctg stg caa tct ggg gct gag gtg aag    155
     211    Gly Ala His Ser Gln Val Xaa Leu Xaa Gln Ser Gly Ala Glu Val Lys
     212                     1                  5                  10
     213    arg cct ggg gcc tcw gtg aag gtc tcc tgy aag rct tct gga tac rcc    203
     214
     215    Xaa Pro Gly Ala Ser Val Lys Val Ser Cys Lys Xaa Ser Gly Tyr Xaa
     216                     15                 20                 25
E-    217    ttc asc gkc tac tat ata cac tgg sts cgm cag gcc cct gga caa ggg    251
     218    Phe Xaa Xaa Tyr Tyr Ile His Trp Xaa Arg Gln Ala Pro Gly Gln Gly
     219             30                 35                 40
     220    ctt gag tgg atg ggw cgg ats aat cct aag gat ggt gcc ccc aac tat    299
     221    Leu Glu Trp Met Gly Arg Xaa Asn Pro Lys Asp Gly Ala Pro Asn Tyr
     222    45                 50                 55                 60
     223    gca ccg aac ttt gaa ggc agg gtc acc atg acc agg gac acg tcc atc    347
     224    Ala Pro Asn Phe Glu Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile
     225             65                 70                 75
     226    acc aca gcg tac at                                                361
     227    Thr Thr Ala Tyr
     228             80
```

```
     229    <210> 101
E--  230    <211> 722
     231    <212> DNA
     232    <213> Homo sapiens
     233    <220>
     234    <221> CDS
```

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        235   <222> 337..720
        236   <221> sig_peptide
        237   <222> 337..408
        238   <223> score 4.2
        239         seq IWSFPLIIAAVCA/QS                    see
                                                            item 10 on Erm Summary Sheet
        240   <400> 101
W-->    241         agaatcagac cgaaacccag agagacagca ttgcctttct gcgtcycctc gcccmmctcs    60
        242         sctcctgcta taaataaccc ggastagcgg gtcaggaacg tcacacggcg agaaaacagg   120
        243         accccgaggt tttcttctct gggaataggg ggcaaagggt gaggagagga gaaagaaatc   180
        244         gctcgaaatc tgctcggtcc ccggcagccg ccgcttcccc tttgacgttt tggtacgccg   240
        245         tgcgcatgcg cctcacatta gaattactgc actgggcaga ctaagttgga tctcctctct   300
        246         tcagtgaaac cctcaattcc atcaaaaact aaaggg atg tgg aga gtg cgg aaa      354
        247                                                Met Trp Arg Val Arg Lys
        248                                                                    -20
        249         arg ggc tac ttt ggg att tgg tcc ttc ccc tta ata atc gcc gct gtc      402
        250
        251         Xaa Gly Tyr Phe Gly Ile Trp Ser Phe Pro Leu Ile Ile Ala Ala Val
        252                     -15                 -10                 -5
E--?K   253         tgt gcg cag agt gtc aat gac cct agt aat atg tcg ctg gtt aaa gag      450,
        254         Cys Ala Gln Ser Val Asn Asp Pro Ser Asn Met Ser Leu Val Lys Glu
        255                      1               5                   10
        256         acg gtg gat aga ctc ctg aaa ggc tat gac att cgt ctg aga cca gat      498,
        257         Thr Val Asp Arg Leu Leu Lys Gly Tyr Asp Ile Arg Leu Arg Pro Asp
        258         15                  20                  25                  30
        259         ttt gga ggt ccc ccc gtg gct gtg ggg atg aac att gac att gcc agc      546
        260         Phe Gly Gly Pro Pro Val Ala Val Gly Met Asn Ile Asp Ile Ala Ser
        261                     35                  40                  45
        262         atc gat atg gtt tct gaa gtc aat atg gat tat acc ttg aca atg tac      594
        263         Ile Asp Met Val Ser Glu Val Asn Met Asp Tyr Thr Leu Thr Met Tyr
        264                     50                  55                  60
        265         ttt caa caa gcc tgg aga gat aag agg ctg tct awa aat gta ata cct      642
        266         Phe Gln Gln Ala Trp Arg Asp Lys Arg Leu Ser Xaa Asn Val Ile Pro
        267                     65                  70                  75
        268         tta aac ttg act ctg gac aac aga gtg gca gac cag ctc tgg gtg cct      690
        269         Leu Asn Leu Thr Leu Asp Asn Arg Val Ala Asp Gln Leu Trp Val Pro
        270                     80                  85                  90
        271         gat acc tat ttc ctg aac gat aag aag tca tt                           722
        272         Asp Thr Tyr Phe Leu Asn Asp Lys Lys Ser
        273         95                  100
```

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        274   <210> 2790
E--?K   275   <211> 462
        276   <212> DNA
        277   <213> Homo sapiens
        278   <220>
        279   <221> CDS                       (next page)
        280   <222> 42..461
        281   <400> 2790          item 10
W-->    282         agttgaaaga ggccatcaag atcctggaga gcctcaagaa c atg act gtg gag cag     56
        283                                                      Met Thr Val Glu Gln
```

```
284                                                    1              5
285        ctg ctg acg ggc tcg ccc acc tct ccg act gtg gag cct gag aag cca    104
286        Leu Leu Thr Gly Ser Pro Thr Ser Pro Thr Val Glu Pro Glu Lys Pro
287                        10              15              20
288        act cgg gag aag aag ttt ctg gat gac atc aag aag cta cag gaa aac    152
289        Thr Arg Glu Lys Lys Phe Leu Asp Asp Ile Lys Lys Leu Gln Glu Asn
290                        25              30              35
291        ctc aag aag acc ctg gac aat gtg gcc att gta gag gag gag aag atg    200
292        Leu Lys Lys Thr Leu Asp Asn Val Ala Ile Val Glu Glu Glu Lys Met
293                        40              45              50
294        gaa gca gtg ccc gac gta gag cgc aag gag gac aag ccc gag ggg cag    248
295        Glu Ala Val Pro Asp Val Glu Arg Lys Glu Asp Lys Pro Glu Gly Gln
296                        55              60              65
297        tca cct gtg aag gtn gag tgg ccc agc gaa acc ccg gtg ctg tgc cag    296
298        Ser Pro Val Lys Xaa Glu Trp Pro Ser Glu Thr Pro Val Leu Cys Gln
299        70              75              80              85
300        cag tgt ggc ggc aag cct ggc gtc acc ttc acc agc gcc aag ggc gag    344
301        Gln Cys Gly Gly Lys Pro Gly Val Thr Phe Thr Ser Ala Lys Gly Glu
302                        90              95              100
303        gtc ttc tcc gta ctg gag ttt gca ccc tca aat cat tct ttt aag aaa    392
304        Val Phe Ser Val Leu Glu Phe Ala Pro Ser Asn His Ser Phe Lys Lys
305                        105             110             115
306        att gag ttc cag cct cca gaa gcc aag aag ttc ttc agc aca gtg cgg    440
307        Ile Glu Phe Gln Pro Pro Glu Ala Lys Lys Phe Phe Ser Thr Val Arg
308                        120             125             130
309        arg gag atg gcg ctg ctg gct a                                      462
310
311        Xaa Glu Met Ala Leu Leu Ala
312                        135             140
```

W--> (lines 297, 329)
E--> (line 314)

```
313        <210> 4101
314        <211> 282
315        <212> PRT
316        <213> Homo sapiens
317        <220>
318        <221> SIGNAL
319        <222> -20..-1
320        <223> score 5
321              seq LQRFAVLSRGVHS/SV
322        <400> 4101
323        Met Phe Ser Lys Leu Ala His Leu Gln Arg Phe Ala Val Leu Ser Arg
324        -20             -15             -10             -5
325        Gly Val His Ser Ser Val Ala Ser Ala Thr Ser Val Ala Thr Lys Lys
326                        1               5               10
327        Thr Val Gln Gly Pro Pro Thr Ser Asp Asp Ile Phe Glu Arg Glu Tyr
328                        15              20              25
329        Lys Tyr Gly Ala His Asn Tyr Xaa Pro Leu Pro Val Ala Leu Glu Arg
330                        30              35              40
331        Gly Lys Gly Ile Tyr Leu Trp Asp Val Glu Gly Arg Lys Tyr Phe Asp
332        45              50              55              60
```

```
       333                Phe Leu Ser Ser Tyr Ser Ala Val Asn Gln Gly His Cys His
       334                            65              70
```

```
       335     <210> 4102
E-->   336     <211> 213  71
       337     <212> PRT
       338     <213> Homo sapiens
       339     <220>
       340     <221> SIGNAL
       341     <222> -20..-1
       342     <223> score 3.5
       343           seq WQLVLNVWGKVEA/DI
       344     <400> 4102
       345           Met Gly Leu Ser Asp Gly Glu Trp Gln Leu Val Leu Asn Val Trp Gly
       346           -20              -15             -10                   -5
       347           Lys Val Glu Ala Asp Ile Pro Gly His Gly Gln Glu Val Leu Ile Arg
       348                           1           5                   10
       349           Leu Phe Lys Gly His Pro Glu Thr Leu Glu Lys Phe Asp Lys Phe Lys
       350               15                  20                  25
       351           His Leu Lys Ser Glu Asp Glu Met Lys Ala Ser Glu Asp Leu Lys Lys
       352               30                  35                  40
       353           His Gly Ala Thr Val Leu Thr
       354           45                  50
```

```
       355     <210> 4103
E-->   356     <211> 339  113
       357     <212> PRT
       358     <213> Homo sapiens
       359     <220>
       360     <221> SIGNAL
       361     <222> -20..-1
       362     <223> score 3.5
       363           seq WQLVLNVWGKVEA/DI
       364     <400> 4103
       365           Met Gly Leu Ser Asp Gly Glu Trp Gln Leu Val Leu Asn Val Trp Gly
       366           -20              -15             -10                   -5
       367           Lys Val Glu Ala Asp Ile Pro Gly His Gly Gln Glu Val Leu Ile Arg
       368                           1           5                   10
       369           Leu Phe Lys Gly His Pro Glu Thr Leu Glu Lys Phe Asp Lys Phe Lys
       370               15                  20                  25
       371           His Leu Lys Ser Glu Asp Glu Met Lys Ala Ser Glu Asp Leu Lys Lys
       372               30                  35                  40
       373           His Gly Ala Thr Val Leu Thr Ala Leu Gly Gly Ile Leu Lys Lys Lys
       374           45                  50                  55                  60
       375           Gly His His Glu Ala Glu Ile Lys Pro Leu Ala Gln Ser His Ala Thr
       376                           65              70                  75
W-->   377           Lys His Lys Ile Pro Val Lys Xaa Xaa Gly Val His Leu Gly Met His
       378                           80                  85                  90
       379           His
```

see item 10

```
       380     <210> 4104
```

```
E-->   381   <211> (324) /08 show
       382   <212> PRT
       383   <213> Homo sapiens
       384   <220>
       385   <221> SIGNAL
       386   <222> -34..-1
       387   <223> score 3.8
       388         seq TLFVFISXGSALG/FK
       389   <400> 4104
       390         Met Ala Ser Glu Phe Lys Lys Lys Leu Phe Trp Arg Ala Val Val Ala
       391                          -30              -25              -20
W-->   392         Glu Phe Leu Ala Thr Thr Leu Phe Val Phe Ile Ser Xaa Gly Ser Ala
       393                      -15              -10              -5
W-->   394         Leu Gly Phe Lys Tyr Pro Val Gly Xaa Asn Gln Thr Ala Val Gln Asp
       395                  1           5               10
       396         Asn Val Lys Val Ser Leu Ala Phe Gly Leu Ser Ile Ala Thr Leu Ala
       397              15              20              25              30
       398         Gln Ser Val Gly His Ile Ser Gly Ala His Leu Asn Pro Ala Val Thr
       399                      35              40              45
W-->   400         Leu Gly Leu Leu Leu Ser Cys Gln Ile Ser Ile Phe Arg Xaa Ser Cys
       401                      50              55              60
       402         Thr Ser Ser Pro Ser Ala Trp Gly Pro Ser Ser Pro
       403                  65              70
```

```
       404   <210> 4105
E-->   405   <211> (348) //6
       406   <212> PRT
       407   <213> Homo sapiens
       408   <220>
       409   <221> SIGNAL
       410   <222> -44..-1
       411   <223> score 5.5
       412         seq ILFFTGWWIMIDA/AV
       413   <400> 4105
       414         Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys Ile
       415                          -40              -35              -30
       416         Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala Gly Ile
       417                      -25              -20              -15
       418         Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala Val Val Tyr
       419                  -10               -5              1
       420         Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr Cys Gly Val Phe
       421         5               10              15              20
       422         Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val Ser Asn Ala Gln Val
       423                      25              30              35
       424         Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu Gly Arg Thr Gly Ala Arg
       425              40              45              50
W-->   426         Val Xaa Leu Phe Ile Gly Phe Met Leu Met Phe Gly Ser Leu Ile Ala
       427              55              60              65
       428         Ser Met Trp Ile
       429              70
```

```
        430    <210> 4106
E-->    431    <211> 300  /00
        432    <212> PRT
        433    <213> Homo sapiens
        434    <220>
        435    <221> SIGNAL
        436    <222> -19..-1
        437    <223> score 6.2
        438          seq WXFLVAIIKGVQC/XX
        439    <400> 4106
W-->    440        --> Met Glu Phe Gly Leu Xaa Trp Xaa Phe Leu Val Ala Ile Ile Lys Gly
        441    Jem -->          -15                 -10                 -5
W-->    442    Jem --> Val Gln Cys Xaa Xaa Xaa Leu Val Glu Ser Gly Gly Xaa Leu Val Lys
        443    /0               1               5                   10
W-->    444    /0  --> Xaa Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        445               15               20                  25
W-->    446        --> Ser Asp Xaa Tyr Met Xaa Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
        447            30               35                  40                  45
W-->    448        --> Glu Trp Val Ser Tyr Ile Ser Ser Gly Gly Xaa Tyr Thr Asn Tyr Ala
        449                             50                  55                  60
W-->    450        --> Asp Ser Xaa Xaa Gly Arg Xaa Xaa Ile Ser Arg Asp Asn Ala Lys Asn
        451                         65                  70                  75
        452            Ser Leu Tyr Leu
        453                80
```

```
        454    <210> 4107
E-->    455    <211> 378  /26  see next page, too
        456    <212> PRT
        457    <213> Homo sapiens
        458    <220>
        459    <221> SIGNAL
        460    <222> -19..-1
        461    <223> score 11.7
        462          seq VFCLLAVAPGAHS/QV
        463    <400> 4107
        464            Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
        465                            -15                 -10                 -5
        466            Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
        467                         1               5                   10
        468            Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        469                15               20                  25
W-->    470        --> Thr Ser Xaa Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Xaa
        471    Jem --> 30               35                  40                  45
W-->    472    Jem --> Glu Trp Met Gly Ile Ile Asn Pro Ser Xaa Gly Ser Thr Xaa Tyr Ala
        473    /0                       50                  55                  60
        474            Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
        475                         65                  70                  75
W-->    476        --> Thr Val Tyr Met Xaa Leu Ser Ser Leu Xaa Ser Xaa Asp Thr Ala Val
        477                80                  85                  90
```

```
W-->   478  Ilen 10   Tyr Xaa Cys Ala Arg Xaa Ala Tyr Ser Ser Tyr Arg Phe Asp
       479            95              100              105
```

```
       480  <210> 4108
E-->   481  <211> 381  /27
       482  <212> PRT
       483  <213> Homo sapiens
       484  <220>
       485  <221> SIGNAL
       486  <222> -19..-1
       487  <223> score 11
       488        seq TLLLLTVPSWVLS/QV
       489  <400> 4108
       490        Met Asp Ile Leu Cys Ser Thr Leu Leu Leu Leu Thr Val Pro Ser Trp
       491                    -15              -10              -5
       492        Val Leu Ser Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys
       493                    1               5               10
       494        Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
       495            15              20              25
W-->   496        Xaa Thr Ser Gly Met Xaa Val Ser Trp Ile Arg Gln Xaa Pro Gly Lys
       497  Ilen 10  30              35              40                  45
W-->   498  Ilen 10  Xaa Leu Glu Trp Leu Ala Xaa Ile Asp Trp Xaa Asp Asp Lys Xaa Tyr
       499                    50              55              60
       500        Ser Thr Ser Leu Lys Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys
       501                    65              70              75
       502        Asn Gln Val Val Leu Thr Leu Ser Lys Met Asp Pro Val Asp Thr Ala
       503                    80              85              90
       504        Thr Tyr Tyr Cys Ala Arg Ser Arg Leu Val Pro His Asp His Trp
       505            95              100             105
```

```
       506  <210> 4109
E-->   507  <211> 264  88
       508  <212> PRT
       509  <213> Homo sapiens
       510  <220>
       511  <221> SIGNAL
       512  <222> -19..-1
       513  <223> score 11
       514        seq TLLLLTVPSWVLS/QV
       515  <400> 4109
       516        Met Asp Ile Leu Cys Ser Thr Leu Leu Leu Leu Thr Val Pro Ser Trp
       517                    -15              -10              -5
W-->   518  Ilen  Val Leu Ser Gln Val Thr Leu Xaa Glu Ser Gly Pro Ala Leu Val Lys
       519  /10            1               5               10
       520        Pro Thr Glu Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu
       521            15              20              25
       522        Asn Val Ser Gly Met Arg Met Ile Trp Val Arg Gln Phe Pro Gly Gln
       523            30              35              40                  45
       524        Ala Leu Glu Trp Leu Ala Arg Ile Asp Trp Asp Asp Glu Lys Tyr Phe
       525                    50              55              60
```

```
        526         Thr Ser Ser Leu Arg Thr Arg Leu
        527                     65
```

```
        528         <210> 4110
E-->    529         <211> 330  //0
        530         <212> PRT
        531         <213> Homo sapiens
        532         <220>
        533         <221> SIGNAL
        534         <222> -19..-1
        535         <223> score 10.6
        536              seq ILFLVAAXTGAXS/QV
        537         <400> 4110
W-->    538         Met Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Xaa Thr Gly
        539                         -15                 -10                 -5
W-->    540         Ala Xaa Ser Gln Val Xaa Leu Xaa Gln Ser Gly Xaa Glu Val Lys Xaa
        541                     1               5               10
W-->    542         Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Xaa Phe
        543                     15              20              25
W-->    544         Xaa Arg Tyr Xaa Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
        545                     30              35              40              45
        546         Glu Trp Met Gly Trp Ile Ser Pro Tyr Asn Gly Asn Thr Asn Tyr Ala
        547                             50              55              60
        548         Gln Gln Phe Gln Asp Arg Val Thr Leu Thr Thr Asp Thr Ser Thr Ser
        549                             65              70              75
        550         Thr Ala Phe Leu Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr
        551                     80              85              90
```

```
        552         <210> 4111
E-->    553         <211> 360  /20    ( see next page, too )
        554         <212> PRT
        555         <213> Homo sapiens
        556         <220>
        557         <221> SIGNAL
        558         <222> -19..-1
        559         <223> score 10.7
        560              seq ILFLVAAATGXHS/QV
        561         <400> 4111
        562         Met Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
        563                         -15                 -10                 -5
W-->    564         Xaa His Ser Gln Val Gln Leu Val Gln Ser Gly Xaa Glu Val Lys Lys
        565                     1               5               10
        566         Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        567                     15              20              25
        568         Thr Ser Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
        569                     30              35              40              45
W-->    570         Glu Trp Met Gly Trp Ile Ser Xaa Tyr Asn Gly Asn Thr Asn Tyr Ala
        571                             50              55              60
W-->    572         Gln Xaa Xaa Gln Gly Arg Val Thr Met Thr Xaa Asp Thr Ser Thr Asn
        573                     65              70              75
```

```
W-->   574  —>   Thr Ala Tyr Met Xaa Leu Arg Xaa Leu Arg Ser Asp Asp Thr Ala Val
       575                80              85              90
W-->   576  —)   Tyr Tyr Cys Ala Xaa Arg Gly Leu
       577                95              100
```

```
       578  <210> 4112
E-->   579  <211> 396 /32
       580  <212> PRT
       581  <213> Homo sapiens
       582  <220>
       583  <221> SIGNAL
       584  <222> -19..-1
       585  <223> score 10.8
       586        seq ILFLVAAATGAHS/QV
       587  <400> 4112
       588        Met Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
       589                    -15             -10             -5
W-->   590  —)   Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Xaa Glu Val Lys Lys
       591                1               5               10
       592        Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
       593                15              20              25
W-->   594  —>   Thr Xaa Tyr Xaa Ile Xaa Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
       595        30              35              40              45
       596        Glu Trp Met Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala
       597                    50              55              60
W-->   598  —)   Gln Xaa Leu Gln Gly Arg Val Thr Met Thr Xaa Asp Thr Ser Thr Xaa
       599                65              70              75
W-->   600  —)   Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Xaa
       601                80              85              90
W-->   602  —)   Tyr Tyr Cys Ala Arg Glu Ile Xaa Val Xaa Xaa Cys Asp Gly Gln Leu
       603                95              100             105
       604        Gly Pro Gly Asn
       605        110
```

```
       606  <210> 4113
E-->   607  <211> 315
       608  <212> PRT
       609  <213> Homo sapiens
       610  <220>
       611  <221> SIGNAL
       612  <222> -19..-1
       613  <223> score 9.5
       614        seq ILXLVAAXTGAHS/QG
       615  <400> 4113
W-->   616        Met Asp Trp Thr Trp Xaa Ile Leu Xaa Leu Val Ala Ala Xaa Thr Gly
       617                    -15             -10             -5
W-->   618        Ala His Ser Gln Gly Gln Xaa Val Gln Ser Gly Ala Glu Val Lys Lys
       619                1               5               10
W-->   620        Pro Gly Ala Ser Val Lys Val Ser Cys Lys Xaa Ser Gly Tyr Thr Phe
       621                15              20              25
```

same types of errors (see next page)

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

All item 12 on Errn Summary Sheet

```
<210> 15
<211> 25
<212> DNA
<213> Artificial Sequence

<400> 15                                                    25
gggaagatgg agatagtatt gcctg
```

```
<210> 16
<211> 26
<212> DNA
<213> Artificial Sequence    item 12

<400> 16                                                    26
ctgccatgta catgatagag agattc
```

FYI

Please Note:
Please ensure that all subsequent artificial/unknown sequences have a suitable explanation in the
<220> - <223> section.